

503/550

FIGURE 503

TGCGGCGCAGTGTAGACCTGGGAGGGATGGGGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGGT
CTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCCTGAGCAGCTTCTTGGGCC
CTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAAGAA
CGTCGTGGGGGTGGTGGTGACCTCACTCCAGAAAACAACCTGCGGACGCTGTCTCTCAGCA
CGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGGGTGTT
TGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGACTATGC
CATCATCTTCACTCAGCTGGAGTTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGTACAGTCT
GACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGCCTGGGCTT
CCTGTACAGTTAGCAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGATCCTTCTGTG
AGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCAGTGTCCACCC
ACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATTCCACAGCA

504/550

FIGURE 504

MGGLLLAAFLALVSVPRQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVTL
TPENNLRITLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIFTQLEF
GDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Important features:**Signal peptide:**

amino acids 1-20

505/550

FIGURE 505

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAATCATCGGGCAGAGGTCTCACA
GCAGCCAAGGAACCTGGGGCCGCTCCTCCCCCTCCAGGCCATGAGGATTCTGCAGTTAATC
CTGCTTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAGGATCATCAAGGGGTTCCAGTGC
AAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTCCGAGAAGACCGGGCTACTCTGTGGGGCG
ACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCGCTACATAGTT
CACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCCACTGAG
TCCTTCCCCACCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGACATCATG
CTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCCCTCTCCTCA
CGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCCAGCCCCCAG
TTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTTGAGCACCAGAAGTGTGAG
AACGCCATACCCCGGCAACATCACAGACCATGGTGTGTGCCAGCGTGCAGGAAGGGGGCAAG
GACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACAGTCTCTTCAAGGCATTATC
TCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACACGAAAGTCTGCAAA
TATGTGGACTGGATCCAGGAGACGATGAAGAACAATTAGACTGGACCCACCCACCACAGCCCA
TCACCCCTCCATTTCCACTTGGTGTGTTGGTTCTGTTCACTCTGTTAATAAGAAACCTTAAGCC
AAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATGCTGTCACTTAATAATC
AACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATCTGCCTTGAAATATTGTGACTCTG
GGAATGACAAACCTGGTTTGTCTCTGTTGTATCCCCAGCCCCAAAGACAGCTCCTGGCCAT
ATATCAAGGTTTCAATAAATATTGCTAAATGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAA

506/550

FIGURE 506

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAHC
LKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITWAV
RPLTLSSRCVTAGTSC LISGWGSTSSPQLRLPHTLRCANITII EHQKCE NAYPGNITDTMVCA
SVQEGGKDCQGD SGGPLVCNQSLQGIISWGQDPCAITRKPGVYTRVKCYVDWIQETMKN

Important features:**Signal peptide:**

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

507/550

FIGURE 507

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAGG
AGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAGCA
CCCAAGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAGGCC
TGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTGTTCCCTGTC
CAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTCAGGGCAGGGGCCCCATCCTT
CCAGGCACCAAGGCCTGGATGGAGACCGAGGACACCCTGGGCGGTGTCTGAGTCCCGAGCCC
GACCATGACAGCCTGTACCACCTCCGCCTGAGGAGGACCAGGGCGAGGAGAGGGCCCCGGTTG
TGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACATCTACCAC
CCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCCGCCCTGTCCCAAGGCCCAGGCTGTTGGGA
CTGGGACCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCACAAAAAAAAAAAA
AAAAAA

508/550

FIGURE 508

MRRLLLVTSLVVVLLWEAGAVPAPKVPIKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVLF
PVQKPPLLTTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEFDHDSLYHFPPEEDQGEERP
RLWVMFNHQVLLGPEEDQDHIYHPQ

509/550

FIGURE 509

GCGGAGCCGGCGCCGGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCCC
ACGAGGCTGCGGCATCCTGCCCTCGGAACAATGGGAAGCTCGGCGCGGAGGTGCTTGGGCCGCG
CTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCGGCCCATGAAAGCGCAGCCATG
GCGGCATCTGCAACATAGAGAAATCTGGGCTTCCACACAACCTCCAGTGCTAACTCAACAGAG
ACTCTCCAACATGTGCCCTTCTGACCATACAAATGAACTTCCAACAGTACTGTGAAACCACCA
AATTCAAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCGGCATCT
AATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTCTACACCC
AAAACAACAAGTGTTTACAGAACACATCTCAGATATCAACATCCACAATGACCGTAACCCAC
AATAGTTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACAACAATATGCATTCTGAAGCA
AAGAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTACGCTGGGAGTT
TTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTTCGGTATCGAACC
ATAGATGAACATGATGCCATCATTTTAAGGAAATCCATGGACCAAGGATGGAATACAGATTGAT
GCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAATATTTCTTTTTTGAAAATA
GTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTAAAGATTCTTCAAGG
TAACAAGGGTTTGGGTTTTGAAATAAACATCTGGATCTTATAGACCGTTCAACAAATGGTTTT
AGCAAGTTCATAGTAAGACAAACAAGTCCTATCTTTTTTTTTTGGCTGGGGTGGGGGCATTGG
TCACATATGACCAGTAATTGAAAGACGTCTCACTGAAAGACAGAATGCCATCTGGGCATACA
AATAAGAAGTTTGTACAGCACTCAGGATTTTGGGTATCTTTTGTAGCTCACATAAAGAACTT
CAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACACAGAAATTATACAATCAAA
CTAGATCTGAAGCATAATTTAAGAAAAACATCAACATTTTTTGTGCTTTAAACTGTAGTAGTT
GGTCTAGAAACAAAATACTCC

510/550

FIGURE 510

MGLGARGAWAALLLGLQLALLGAHESAAMAASANIENSGLEPHNSSANSTETLQHVPSDHT
NETSNSTVKPPPTSVASDSSNTTVTTMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQNTS
QISTSTMTVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIGCKM
YYSRRGIRYRTIDEHDAII

FIGURE 511

[illegible]

512/550

FIGURE 512

MARMSFVIAACQLVLGLLMTSLTESSIQNSECPQLCVCEIRPWFTPQSTYREATTVDCNDLRL
TRIPSNLSSDTQVLLQSNNIAKTVDELQQLFNLTDELDFSQNNFTNIKEVGLANLTQLTTLHL
EENQITEMTDYCLQDLNLQELYINHNQISTISAHAFAGLKNLLRLHLNSNKLKVIDSRWFDS
TPNLEILMIGENPVIGILDMNFKPLANLRSLVLAGMYLTDIPGNALVGLDSLESLSFYDNKLV
KVPQLALQKVPNLKFLDLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSVDRYALDNLPELT
KLEATNNPKLSYIHRLAFRSVPALLESMLNNNALNAIYQKTVESLPNLREISIHSNPLRCDCV
IHWINSNKTNIRFMEPLSMFCAMPPEYKKGHVKEVLIQDSSEQCLPMISHDSFPNRLNVDIGT
TVFLDCRAMAEPEPEIYWVTPIGNKITVETLSDKYKLSSEGTLEISNIQIEDSGRYTCVAQNV
QGADTRVATIKVNGTLLDGTQVLKIYVKQTESHSILVSWKVNSNVMTSNLKWSSATMKIDNPH
ITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVTTKNAAFVAVDISDQETST
ALAAVMGSMFAVISLASIAVYFAKRFKRKNYHHS LKKYMQKTSSIPLNELYPPLINLWEGDSE
KDKDGSADTKPTQVDTSRSYMW

Important features:**Signal peptide:**

Amino acids 1-25

Transmembrane domain:

Amino acids 508-530

N-glycosylation sites:Amino acids 69-73;96-100;106-110;117-121;385-389;517-521;
582-586;611-615**Tyrosine kinase phosphorylation site:**

Amino acids 573-582

N-myristoylation sites:

Amino acids 16-22;224-230;464-470;637-643;698-704

513/550

FIGURE 513

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC
CAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT
GTCTGGATGGGCGGCCAGCGATGACCCCATTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT
GAGCAATGCAGAGAGAGAGGTTGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGCATGC
CGGAAGGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA
GTTGGACAAGGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT
GGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAAATGC
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA
CACGCCTTTCATCAACCTTCCC GCCCTGTGGAGGAGCGTCGCCAACATCATGCCCTTAAACTGG
CATCCGGCCTTGCTGGGAGAATAATGTGCCGTTGTACATCAGCTGACATGACCTGGAGGGG
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTGGGATTTGTGAATAAA
CTTGATACACCA

514/550

FIGURE 514

MHLARLVGSCSLLLLLGGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHVNNAAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP

Important features:**Signal peptide:**

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

515/550

FIGURE 515

CCCACGCGTCCGCCACGCGTCCGGGTGCCACTCGCGCGCCGGCCGCGCTCCGGGCTTCTCTT
TTCCCTCCGACGCGCCACGGCTGCCAGACATTCCGGCTGCCGGGTCTGGAGAGCTCCCCGAA
CCCTCCGCGGAGAGGAGCGAGGCGCGCCAGGGTGGCCCCCGGGGCGCGCTTGGTCTCGGAG
AAGCGGGGACGAGGCGCGAGGATGAGCGACTGAGGGCGACGCGGGCACTGACGCGAGTTGGGG
CCGCGACTACCGGCACTGACAGCGCGATGAGCGACTCCCCAGAGACGCCCTAGCCCCGTGTG
CGCGCCAGGCGGAGCGCGCAGGTGGGGCTGGGCTGTTAGTGGTCCGCCCCACGCGGGTCCCGG
GCCGCCCCAGGATGGGCGCTGGCAACCGGGCCCCGCGCCGCCGCTGCTACCCCTGCGCCCCG
TGCGAGCCCCGGCGTCCGCCCCGCGCCCTGCGCTCATGGACGGCGCTCCCGCTGCGCGCGGC
GCGCCCCCGGGCTGTGAATGCGACTCGCCCCCTCGGCCGCGCTCCCCGCCCGCCCCCGCCGG
GACGTGGTAGGGGATGCCAGCTCCACTGCGATGGCAGTTGGCGCGCTCTCCAGTTCCCTCCT
GGTCACCTGCTGCTGTAGTGGTGGCTCTGTGCAGTCCGAGCATCCCGTGGAGAAGCTGGCCCA
GGCACAGAGCAGCCGGCCAGGAGAAGCGTGAGCACGCCACTCGGGACGCGCCCGGGGCGGGT
GAACGAGCTCGGGCGCCCGGCGAGGACGAGGGCGGCGAGCGCCGGGACTGGAAGAGCAAGAG
CGGCCGTGGGCTCGCGCGCCGTGAGCCGTGGAGCAAGCTGAAGCAGGCCTGGGTCTCCAGGG
CGGGGGCGCCAAGGCCGGGGATCTGCAGGTCCGGCCCCGCGGGGACACCCCGCAGCGCGAAGC
CCTGGCGCGACGCGCCCGAGGACGCGATTGGCCCGAACTCGCGCCACGCGCCGAGCCACCCGA
GGAGTACGTGTACCCGGACTACCGTGGCAAGGGCTGCGTGGACGAGAGCGGCTTCGTGTACGC
GATCGGGGAGAAGTTCGCGCGCGGCCCTCGGCCTGCCCGTGCCTGTGCACCGAGGAGGGGCC
GCTGTGCGCGAGCCGAGTGCCCGAGGCTGCACCCGCGCTGCATCCAGCTGCACACGAGCCA
GTGCTGCCCGCAGTGCAAGGAGAGGAAGAACTACTGCGAGTTCGGGGCAAGACCTATCAGAC
TTTGGAGGAGTTCGTGGTGTCTCCATGCGAGAGGTGTCGCTGTGAAGCCAACGGTGAGGTGCT
ATGCACAGTGTACGCGTGTCCCCAGACGGAGTGTGTGGACCTGTGTACGAGCCTGATCAGTG
CTGTCCCATCTGCAAAAATGGTCCAACTGCTTTGCAGAAACCGCGGTGATCCCTGCTGGCAG
AGAAGTGAAGACTGACGAGTGCACCATATGCCACTGTACTTATGAGGAAGGCACATGGAGAAT
CGAGCGGCAGGCCATGTGCACGAGACATGAATGCAGGCAAACTAGACGCTTCCAGAACACA
AACTCTGACTTTTCTAGAACATTTTACTGATGTGAACATTCTAGATGACTCTGGGAACATC
AGTCAAAGAAGACTTTTGATGAGGAATAATGGAAAATTTGTTGGTACTTTTCTTTTCTTGATA
ACAGTTACTACAACAGAAGGAAATGGATATATTTCAAACATCAACAAGAACTTTGGGCATAA
AATCCTTCTCTAAATAAATGTGCTATTTTCACAGTAAGTACACAAAAGTACACTATTATATAT
CAAATGTATTTCTATAATCCCTCCATTAGAGAGCTTATATAAGTGTTTTCTATAGATGCAGAT
TAAAAATGCTGTGTGTCAACCGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

516/550

FIGURE 516

MPSSTAMAVGALSSSLVTCCLMVALCSPSIPLEKLAQAFEPGQEKREHATRDGPGRVNELG
RPARDEGGSGRDWKS KSGRGLAGREPWSKLKQAWVSQGGGAKAGDLQVRPRGDT PQAEALAAA
AQDAIGPELAPTPEPPPEYVYPDYRGKGCVDSESGFVYAIGKFAFGPSACPLCTEEGPLCAQ
PECPRLHPRCIHVDTSQCCPQCKERNKYCEFRGKTYQTLEEFVVS PCERCRC EANGEVLCTVS
ACPQTECVDPVYEPDQCCPICKNGPNCFAETAVIPAGREVKTDECTICHCTYEEGTWRIERQA
MCTRHECRQM

Important features:**Signal peptide:**

amino acids 1-27

Transmembrane domain:

amino acids 11-30

Glycosaminoglycan attachment site.

amino acids 80-83

N-myristoylation sites.

amino acids 10-15, 102-107, 103-108

Cell attachment sequence.

amino acids 114-117

EGF-like domain cysteine pattern signature.

amino acids 176-187

517/550

FIGURE 517

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCCT
TTCGGCCTTGAGGTTCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCTAC
GGACGACGCCTATGAAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTGTGC
CGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATACAAG
TTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAAATCTAACT
CTCCAAAACATGTTTATCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTACACATG
GAGACGCTTCAACTGAGAATGATGTTTAAACCAATCCTATCAGTGAAGAAACTACAACTTTCC
CTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCCATTTCTGGT
CGATCAAAACCAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTGAAAATGAAG
AGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAAACTGAGGCACCAAGAATGTTGCCAGTTG
TTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAACCACTTTAGATA
AGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCTCAGCTCTCAGGTGAAACTG
CGATAGAAAAACCGAAGAGTTTGGAAAGCACCCAGAGAGTTGGAATAATGATGACATTTTGA
AAAAAATTTTAGATATTAATTCAAGTGCAACAGGCCTTCTTAGTGACACCAGCAACCCAG
CATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCCTTGCTCTAGCAGCAG
CAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCAGTAGGACGAACAAGTA
ATAAAATTTGATGACATCGAAACTGTTATTAACATGCTGTGTAATTCTAGATCTAAACTCTATG
AATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAGCTGCTACAGTATTCAATA
CATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTAAGGTTTATTAAACAATAA
TATAAAAAATTTAAACCTACTTGATATTCCATAACAAAGCTGATTTAAGCAAACCTGCATTTTT
TCACAGGAGAAATAATCATATTTCGTAATTTCAAAGTTGTATAAAAAATTTTTCTATTGTAGT
TCAAATGTGCCAACATCTTTATGTGTCATGTGTTATGAACAATTTTCATATGCACATAAAACC
TAATTTAAAAATAAAATTTTGGTTCAGGAAAAA

518/550

FIGURE 518

MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSVPSGEPGREKKSNSPKH
VYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTGGFTPEIGKKKHTESTPFWSIKP
NNVSIVLHAEPEYIENEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDKSTG
IEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSVQQALLSDTSNPAYRE
DIEASKDHLKRSLALAAAAEHKLKTMYSQQLLPVGRTSNKIDDIETVINMLCNSRSKLYEYLD
IKCVPPPEMREKAATVFNTLKNMCRSRRVTALLKVY

Important features:**Signal peptide:**

amino acids 1-19

519/550

FIGURE 519

CGGCTCGAGTGCAGCTGTGGGGAGATTTTCAGTGCATTGCCTCCCTGGGTGCTCTTCATCTTG
GATTTGAAAGTTGAGAGCAGCATGTTTTGGCCACTGAAACTCATCTGCTGCCAGTGTTACTG
GATTATTTCTTGGGCCTGAATGACTTGAATGTTTCCCCGCTGAGCTAACAGTCCATGTGGGT
GATTACAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAGATAGAC
TGGACTCTGTCAACAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCAATCTC
AGTGTGCCTATTGGGCGCTTCCAGAACC CGTACACTTGATGGGGACATCTTATGCAATGAT
GGCTCTCTCCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGAAATCCGC
CTCAAAGGGGAGAGCCAGGTGTTCAAGAAGCGGTGGTACTGCATGTGCTTCCAGAGGAGCCC
AAAGAGCTCATGGTCCATGTGGGTGGATTGATTCAGATGGGATGTGTTTTCCAGAGCACAGAA
GTGAAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCGCAAAGGAGGAGATTGTA
TTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGGGCCACTTCCAG
AATCGTGTGAACCTGGTGGGGGACATTTTCCGCAATGACGGTTCCATCATGCTTCAAGGAGTG
AGGGAGTCAGATGGAGGAAACTACACCTGCAGTATCCACCTAGGGAACCTGGTGTTCAAGAAA
ACCATTTGTGCTGCATGTGCAGCCCGAAGAGCCTCGAACACTGGTGACCCCGGCAGCCCTGAGG
CCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTGTGGGAATTGTCTGTGCCACAATCCTG
CTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAATAAGAGTTCAGTGAATTCT
ACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAAGAAAAACCTGCCATTTT
GAAAGATGTGAAGGGGAGAAACACATTTACTCCCCAATAATGTACGGGAGGTGATCGAGGAA
GAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCACCCAGTTTGGCCTTCTCTG
AGGTGAGATCGGAACAACTCACTTGAAAAAAGTCAGGTGGGGGAATGCCAAAAACACAGCAA
GCCTTTTGAGGAAGAATGGAGAGTCCCTTCATCTCAGCAGCGGTGGAGACTCTCTCTGTGTGT
GTCTTGGGCCACTCTACCAAGTGATTTTCAGACTCCCGCTCTCCAGCTGTCTCTCTGTCTCATT
GTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGGCAGAGAGACTGGACAGCTCTGGA
GGAACAGGCCTGCTGAGGGGAGGGGAGCATGGACTTGGCCTCTGGAGTGGGACACTGGCCCTG
GGAACAGGCTGAGCTGAGTGGCCTCAAACCCCGTTGGATCAGACCTCTCTGTGGGCAGGG
TTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATAAAACCAACCCAAATCAA

520/550

FIGURE 520

MFCPLKLILLPVLLDYSGLNDLNVSPPELTVHVGDSSALMGCVFQSTEDKCIFKIDWTLSFGE
HAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGESQV
FKKAVVLHVLFEETPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKL
RMSVEYSQSWGHFQNRVNLVGDI FRNDGSIMLQGVRES DGGNYTCSIHLGNLVFKKTI VLVHS
PEEPRTLVT PAALRPLVLGGNQLV IIVGIVCATILLLPVLILIVKKT CGNKSSVNSTVLVKNT
KKTNP EIKEKPCHFERCEGEKHIYSPIIVREVIEEEE PSEKSEATYMTMHPVWP SLRSDRNN S
LEKKSGGGMPKTQQAF

521/550

FIGURE 521

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATGG
TTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGGAA
ACTACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCAGGA
TGAAGATGGATACATCACCTTAAATATTTAAAACTCGGAAACCAGCTCTCGTCTCCGTTGGCCC
TGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGGATGGT
TGTCGGGCTGGTGGCTCTGGGGATTTGGTCTGTTCATGCAGCGCAATTACCTACAAGATGAGAA
TGAAATCGCACAGGAACCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGGTAAAACA
ATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCTGTGACACAACTGGAGATA
TTATGGAGATAGCTGCTATGGGTCTTTCAGGCACAACCTAACATGGGAAGAGAGTAAGCAGTA
CTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGGAGTACATCAA
AGCCAGGACTCATTTAAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAATGAGGTCTGGAA
GTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTTGGAAGATGGAAAAGGAAA
TATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTGAGAACAAACATTA
TTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCTTAATGCAAAGAGGT
GGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGTATGAATGCATCAGTA
GCTGAAAAAAAAAAAAA

522/550

FIGURE 522

MQDEDEGYITLNIKTRKPALVSVGPASSSSWVRVMALILLILCVGMVVGLVALGIWSVMQRNYLQ
DENENRTGTLQQLAKRRCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLTWEEES
KQYCTDMNATLLKIDNRNIVEYIKARTHLIRWVGLSRQKSNEVWKWEDGSVISENMFEELEDG
KGNMNCAYFHNGKMHPTFCENKHLYLMCERKAGMTKVDQLP

523/550

FIGURE 523

CAGCAGTGGTCTCTCAGTCCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATG**GC
AAAGAATCCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCCAA
GAAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTTTGGTATCTGGCCCTAACTCTAAT
TGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACATGGA
GCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTGACCAG
AACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTTTAAAAA
CGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGATTAAAGT
GATTCCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACCACAACTTT
CTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGATTTTCTTAA
AAATTCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATCCCACTCTAAT
ATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTTCTTGCCAACGA
AAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGTAGAGAAGACCCG
TCACGCCAGACAAGCAAGTGAGGAAGAACTTCCAATAAATGACTATACTGAAAAATGGAATAGA
ATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGTCGAGGCAACCGCTA
TTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATACTGCTACCAAGGAGG
ACGAGTCATCTGTCGTGTCATCATGCCTTGTAAC TG GTGGGTGGCCCGCATGCTGGGGAGGGT
CTAATAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATATAATAAATGCATGCTATT
CAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCTCTCCAGAATTACTTGTAG
GTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACCAAAAAAAAAAAAAAAAAA

524/550

FIGURE 524

MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALTIVLFWGSKHFWPEVPKKAYD
MEHTFYSNGEKKKIYMEIDPVTREIFRSGNGTDETLVHDFKNGYGTGIYFVGLQKCFIKTQI
KVIPEFSEPEEEIEDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWINPT
LISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDYTENG
IEFDPMLDERGYCCIYCRGRNRYCRRVCEPLLGYYPYPYCYQGGRVICRVIMPCNWWWARMLGRV

Important features:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

525/550

FIGURE 525

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAAGATCACTGGGGGTC
TCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCCAA
AAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCACAT
ACCTACCAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACCTGTGTACCGAGA
GCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCATGGAC
ATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTGAGTTTC
TTTCAGTTTTACTGATGTTCTGGGTGGGGGACAGAGCCAGATTCAGAGTAATCTTGACTGAAT
GGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCATTTTTTTTTT
TAACACGTCATAAAAAAATAATCTCCAGA

526/550

FIGURE 526

MKITGGLLLLCTVVYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGNE
CHLCTESLKSNQGRVQFLHDGSC

Important features:

Signal peptide:

amino acids 1-19

527/550

FIGURE 527

CGACGATGCTACGCGCGCCCGGCTGCCTCCTCCGGACCTCCGTAGCGCCTGCCGCGGCCCTGG
CTGCGGCGCTGCTCTCGTCGCTTGCGCGCTGCTCTCTTCTAGAGCCGAGGGACCCGGTGGCCT
CGTCGCTCAGCCCCATTTCCGACCAAGACTCGCTACGAGGATGTCAACCCCGTGCTATTGT
CGGGCCCGAGGCTCCGTGGCGGGACCTGAGCTGCTGGAGGGGACCTGCACCCCGGTGCAGC
TGGTCGCCCTCATTCGCCACGGCACCCGCTACCCACGGTCAACACATCCGCAAGCTGAGGC
AGCTGCACGGGTTGCTGCAGGCCCCGGGTTCCAGGGATGGCGGGGCTAGTAGTACCCGGACGC
GCGACCTGGGTGCAGCGCTGGCCGACTGGCCTTTGTGGTACGCGGACTGGATGGACGGCGAGC
TAGTAGAAGAGGGACGGCAGGATATGCGACAGCTGGCGCTGCGTCTGGCCTCGCTCTCCCGG
CCCTTTTCAGCCGTGAGAACTACGGCCGCTGCGGCTCATCACCAGTTCCAAGCACCGCTGCA
TGGATAGCAGCGCCGCTTCCGTGCAGGGGCTGTGGCAGCACTACCACCTGGCTTGGCCGCGC
CGGACGTGCGAGATATGGAGTTTGGACCTCCAACAGTTAATGATAAACTAATGAGATTTTTTG
ATCACTGTGAGAAGTTTTTAAGTGAAGTAGAAAAAATGCTACAGCTCTTTATCAGCTGGAAG
CCTTCAAACTGGACAGAAATGCAGAACATTTTAAAAAAGTTGCAGCTACTTTGCAAGTGC
CAGTAAATGATTTAAATGCAGATTTAATTCAGTAGCCTTTTTCACCTGTTCAATTGACCTGG
CAATTAAAGGTGTTAAATCTCCTTGGTGTGATGTTTTGACATAGATGATGCAAGGTATTAG
AATATTTAAATGATCTGAAACAATATTGGAAAAGAGGATATGGGTATACATTTAACAGCTCGAT
CCAGCTGCACCTTGTTTCAGGATATCTTTCAGCACTTGGACAAGCAGTTGAACAGAAACAAA
GGTCTCAGCCAATTTCTCTCCAGTCATCTCCAGTTTGGTCATGCAGAGACTCTTCTCCAC
TGCTTTCTCTCATGGGCTACTTCAAAGACAAGGAACCCCTAACAGCGTACAAATTACAAAAAAC
AAATGCATCGGAAGTTCGGAAGTGGTCTCATTTGTACCTTATGCTCGAACCTGATATTTGTGC
TTTACCACGTGAAAAATGCTAAGACTCCTAAAGAACAATTCGAGTGCAGATGTTATTAATG
AAAAGGTGTTACCTTTGGCTTACTCACAAGAACTGTTTCATTTTATGAAGATCTGAAGAAC
ACTACAAGGACATCCTTCAGAGTTGTCAAACAGTGAAGAATGTGAATTAGCAAGGGCTAAACA
GTACATCTGATGAATATGAGTAAGTGAAGAACATTTTAAATCTTTAGGAATCTGCAATGAG
TGATTACATGCTTGAATAGGTAGGCAATTCCTTGATTACAGGAAGCTTTTATATTACTTTGAG
TATTTCTGCTTTTCACAGAAAACATTTGGGTTTCTCTCTGGGTTTGGACATGAAATGTAAGA
AAAGATTTTTCACCTGGAGCAGCTCTCTTAAAGGAGAAACAATCTATTTAGAGAAACAGCTGGC
CCTGCAAATGTTTACAGAAATGAAATTCCTCTACTTATATAAGAAATCTCAGACTGAGATAG
AATTTGATTTTCATAATAACACTTGAAGTGTCTGGAGTAACAAAATATCTCAGTTGGACCAT
CCTTAATCTGATTGAAGTGTCTAGGAATTTACAGATGTTCTGCACTTCTCTCTCTTTCTTCC
TCAGTAGGACAGCTCTAGCAATTTTCTAATCAGGAATATTGTTGGTAAGCTGGGAGTATCACT
CTGGAAGAAAGTAACATCTCCAGATGAGAATTTGAAACAAGAAACAGAGTGTGTAAGGAC
ACCTTCACGAAGCAAGTCGGAAGTACAATGAAAATAAATATTTTGGTATTTTATTTATGAA
ATATTTGAACATTTTTCAATAATTCCTTTTTACTTCTAGGAAGTCTCAAAAGACCATCTTAA
ATTATTATATGTTTGGACAATTAGCAACAAGTGCAGATAGTTAGAATCGAAGTTTTTCAATCC
ATTGCTTAGCTAATTTTTCACTTCTGCTCACTTGCTTGCATTTTATATTTTCCATTTTATATG
AAATGTATCTTTTGGTTGTTGATTTTTCTTCTTTCTTTGTAAATAGTTCTGAGTTCTGTCA
AATGCCGTGAAAGTATTGCTATAATAAAGAAAATCTTGTGACTTTAAAAA

528/550

FIGURE 528

MLRAPGCLLRTSVAPAAALAAALLSSLARCSLLEPRDPVASSLSPYFGTKTRYEDVNPVLLSG
PEAPWRDPELLEGTCTPVQLVALIRHGTRYPTVKQIRKLRQLHGLLQARGSRDGGASSTGSRD
LGAALADWPLWYADWMDGQLVEKGRQDMRQLALRLASLFPALFSRENYGRLRLITSSKHRCMD
SSAAFLQGLWQHYHPGLPPPDVADMEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYHVEAF
KTGPQMQLNLLKKVAATLQVPVNDLNADLIQVAFFTCSPDLAIGVKSPWCDVFDIDDAKVLEY
LNDLKQYWKRQYGYTINSRSSCTLFQDIFQHLDKAVEQKQRSQPISSPVILQFGHAETLLPLL
SLMGYFKDKEPLTAYNYKKQMRKFRSGLIVPYASNLI FVLYHCENAKTPKEQFRVQMLLNEK
VLPLAYSQETVSFYEDLKNHYKDILQSCQTSEECELARANSTSD

Important features:**Signal sequence**

amino acids 1-30

N-glycosylation sites.

amino acids 242-246, 481-485

N-myristoylation sites.

amino acids 107-113, 113-119, 117-123, 118-124, 128-134

Endoplasmic reticulum targeting sequence.

amino acids 484-489

529/550

FIGURE 529

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCTGGAGGTGCCACCCGGCGCGGGTGG
CGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGGGA
CGCGGCGGCGCGGCGGCGGACTGCAGTGGCTGGACGATGGCAGCGTCCGCCGGAGCCGGGGCG
GTGATTGCGAGCCCCAGACAGCCGGCGCTGGCTGTGGTCGGTGTGGCGGCGGCGCTTGGGCTC
TTGACAGCTGGAGTATCAGCCTTGGAAAGTATATACGCCAAAAGAAATCTTCGTGGCAATGGT
ACACAAGGGAAGCTGACCTGCAAGTTCAGTCTACTAGTACGACTGGCGGGTTGACCTCAGTC
TCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCGTTTTTCCACTACTCCCAAGGG
CAAGTGTACCTTGGGAATTATCCACCATTTTAAAGACAGAATCAGCTGGGCTGGAGACCTTGAC
AAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACCTATATCTGT
GATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTATGTCGTAGAA
AAAGAGAATTTGCCTGTGTTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTGCTGTGGTCCTA
GGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCTCTATAGAAGGAAAACTCTAAACGG
GATTACACTGGCTGCAGTACATCAGAGAGTTTGTCAACAGTTAAGCAGGCTCCTCGGAAGTCC
CCCTCCGACACTGAGGGTCTTGTAAAGAGTCTGCCTTCTGGATCTCACCAGGGCCAGTCATA
TATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAACAAGTCAGAGTCTGTG
GTGTATGCGGATATCCGAAAGAATTAAAGAGAATAACCTAGAACAATATCCTCAGCAAGAAACAAA
ACCAAACTGGACTCTCGTGCAGAAAATGTAGCCCATTAACACATGTAGCCTTGGAGACCCAGG
CAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGTACAAAGGATATGTATAAA
TATTTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTGCATGTAGAAAGATGGTATGATTC
TACATATGTACCCATTGTCTTGTCTTTTTGTACTTTCTTTTCAGGTCATTTACAATTGGGAG
ATTTTCAGAAACATTCCTTTCCACCATCATTAGAAATGGTTGCCTTAATGGAGACAATAGCAG
ATCCTGTAGTATTTCCAGTAGACATGGCCTTTAATCTAAGGGCTTAAGACTGATTAGTCTTA
GCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAAGCATACCCAGGGTGGCCTTTAGC
ACAGTATCAGTACCATTTATTTGTCTGCCGCTTTAAAAAATACCCATTGGCTATGCCACTTG
AAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACTAAAATATGGGGCAATTGTTAGCCTT
ACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTGAAATGTGTATATCAATTTCTGGATT
CATAATAGCAAGATTAGCAAAAGGATAAATGCCGAAGGTCACCTTCATTCTGGACACAGTTGGAT
CAATACTGATTAAGTAGAAAATCCAAGCTTGTCTTGAGAACTTTGTAACGTGGAGAGTAAAA
AGTATCGGTTTTTA

530/550

FIGURE 530

MAASAGAGAVIAAPDSRRWLWSVLAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKST
STTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDKKDASINIENMQ
FIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLISMILAV
LYRRKNSKRDTGCGSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSGGHHS
DKINKSESVVYADIRKN

Important features:**Signal peptide:**

amino acids 1-37

Transmembrane domain:

amino acids 161-183

531/550

FIGURE 531

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCGA
GGCTGGTGGGAAGAAGCCGAGATGCGCGGCAGCCAGCGCTGGGGCAACCCGGGTGCTCCTGCTC
TTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCCGGGGCAGCGGCTGCCGGCCGGGACTGGT
GCGCGAGGGGCTGGGGCGAAGGTCGAGAGGGCGAGGCCGTGTGGCAGCGTGCGGGCTGCTGCTG
GAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCTGGAAC
CAGCAGGATGGTACCTTGTCCTGTTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGCCGACTC
CGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGCGACCCGGGGCCCTG
GATGGCCTGGAAGCTGGTGGCTAIGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGGTGGAGTCG
CACCTGTCGGACCAGCTGACCTGTCACGTGGATGTGGCCGGCAACGTGGTGGGCGTGTGCGTG
GTGACGCACCCCCGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGAGCTGTTCAAC
ACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGGCTTCATTGAG
CGCCTGGAGATGGAACAGGCCCGAGAAGGCCAAGAACCCCGAGGAGCAGAAGTCCTTCTTCGCC
AAATACTGGATGTACATCATTTCCCGTCGTCTGTTCCCTCATGATGTGAGGAGCGCCAGACACC
GGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCCTTTGCTGTGTGCCA
CCCTCCCTGTAAAGTCTATTTAAAAACATCGACGATACATTGAAATGTGTGAACGTTTTGAAAA
GCTACAGCTTCCAGCAGCCAAAAGCAACTGTGTTTTGGCAAGACGGTCCTGATGTACAAGCT
TGATTGAAATTCAGTCTCACTTGATACGTTATTCAGAAACCAAGGAATGGCTGTCCCCATC
CTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTATTAAACTGTCCCCAGATC
GACACGCAAAAAAAAAA

532/550

FIGURE 532

MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEID
DSANFRKRGSLLWNQQDGTLSLSQRQLSEEEERGRLRDVAALNGLYRVRIPRRPGALDGLEAGG
YVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQLQP
PTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWYIIPVVLFLMMSGAPDTGGQGGGG
GGGGGGGSGLCCVPPSL

Important features:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 226-243

534/550

FIGURE 534

MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPGCHCGLGGRGQPKDATDWC
CQTHDCCYDHLKTQCGGIYKDNNKSSIHCMDLSQRYCLMAVFNVIYLENEDSE

Important features:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

535/550

FIGURE 535

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGAGCTCTGTGGCTG
AACTGGGTGCTCATCAGCGGAATGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAGCC
CCAAATTGCTTGGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTGTAGGATCCAGTTTTT
TTTTTAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATATCCAT
GAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATTTATTT
GTTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCTCCCAAG
GGGTCCAATTTTTCTTCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGTGCACAGGGG
CTGTCATGCAACTGGCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTGAACAATACAA
AGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTTATAGCCCCC
ACTGTCCTACTGACAATGCTTTCTTCTGCCGAACGAGGATGCCCTAAGGGCTGTAGGTGTGAA
GGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCTCAAGTATATCTGCTGGT
TGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAACTTAAGTATAATCAATTTAAAGGG
CTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATATTGACGAAAATGCT
TTAATGGAATACGACAGCTCAAAGAGCTGATTCTTAGTTCCAATAGAATCTCCTATTTCTT
AACAAATACCTTCAGACCTGTGACAAATTTACGGAACCTGGATCTGTCTTATAATCAGCTGCAT
TCTCTGGGATCTGAACAGTTTTCGGGGCTTGCAGGAGCTGCTGAGTTTACATTTACGGTCTAAC
TCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACCTGGAACCTTTTGGACCTG
GGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCCTTGTCTGGCATGATCAGACTCAAGAA
CTTCACCTGGAGCACAATCAATTTTCCAAGCTCAACCTGGCCATTTTCCAAGGTTGGTCAGC
CTTCAGAACCTTTACTTGCAGTGGAAATAAAATCAGTGTCATAGGACAGACCATGTCTTGACC
TGGAGCTCCTTACAAAGGCTTGATTTATCAGGCAATGAGATCGAAGCTTTCAGTGGACCCAGT
GTTTTCCAGTGTGTCCCGAATCTGCAGCGCCTCAACCTGGATTCCAACAAGCTCACATTTATT
GGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACATCAGTCTTGCTGGGAATATATGG
GAATGCAGCAGAAATATTTGCTCCCTTGTAACCTGGCTGAAAAGTTTTAAAGGTCTAAGGGAG
AATACAATTATCTGTCCAGTCCCAAGAGCTGCAAGGAGTAATGTGATCGATGCAGTGAAG
AACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGTTTGATCTGGCCAGGGCTCTCCCAAG
CCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCATGAGAGCAAAACCCCTTTGCCCCGAGC
GTGGGAGCCACAGAGCCCGGCCACAGAGCCGATGCTGACGCCGAGCACATCTCTTTCCATAAA
ATCATCGCGGGCAGCGTGGCGCTTTTCTGTCCGTGCTCGTCATCTCGTGTGGTTATCTACGTG
TCATGGAAGCGGTACCTCGCAGCATGAAGCAGCTGCGACAGCGCTCCCTCATGCCAAGGCAC
AGGAAAAAGAAAAGACAGTCCCTAAAGCAATGACTCCAGCACCAGGAATTTTATGTAGAT
TATAAACCCACCAACAGCGAGACCAGCGAGATGCTGCTGAATGGGACGGGACCTGCACCTAT
AACAAATCGGGCTCCAGGGAGTGTGAGGTAAGAACCATTTGTGATAAAAAGCTCTTAAAGC
TGGGAATAAGTGGTGCTTTATGAACTCTGGTGACTATCAAGGGAACGCGATGCCCCCCCTC
CCCTTCCCTCTCCCTCTCACTTTGGTGGCAGATCCTTCCCTTGTCCGTTTGTAGTGCAATCATA
ATACTGGTCATTTTCTCTCATACATAATCAACCCATTGAAATTTAAATACCAATCAATGT
GAGGCTTGAACCTCGGTTTAAATATAATACCTATTGTATAAGACCCCTTACTGATTCCATTAAT
GTCGCATTTGTTTTAAGATAAACTCTTTCATAGGTAAGAAAAA

536/550

FIGURE 536

MGFNVIRLLSGSAVALVIAPT VLLTMLSSAERGCPKGCRCCEGMVYCESQKLQEIPSSISAGC
LGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYFLN
NTFRPVTNLRLNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELLDLG
YNRIRSLARNVFAGMIRLKLHLEHNQFSKLNLA LFPRLVSLQNL YLQWNKISVIGQTMSWTW
SSLQRLDLSGNEIEAFSGPSVFPQCVPNLQRLNLD SNKLTFIGQEILDSWISLNDISLAGNIWE
CSRNICSLVNWLSFKGLRENTIICASPKE LQGVNVIDAVKNYSICGKSTTERFDLARALPKP
TEKPKLPRPKHESKEPLPETVGATEPGPETDADA EHISFHKIIAGSVALFLSVLVILLVIYVS
WKRYPASMQLQQRSLMRHRHKKRQSLKQMT PSTQEFYVDYKPTNTETSEMLLNGTGPC TYN
KSGSRECEV

Important features:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

537/550

FIGURE 537

GGGACTACAAGCCGCGCGCGCTGCCGCTGGCCCTCAGCAACCCCTCGACATGCGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCGGCTCGGCTGCCTGACTCTTCTCTGCTGCTGCTTTTCAGGGGCTGCTGATAGGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCAGTGGTACAGGAATTGAAAGTGTGGAAGCTCTTGGATCATCTTACGGATTCCG
AGCAAGTGCACCCAGGATCGAGTGGGAAGAAATTCAGATGAACAAACCACTATGTGTTTGTGACACAAAA
TTCAGGAGACTTGGCGGCTGTGCGAATACTGGGGAAGACATCCCTGAAGATCTGGAATTGTGACACCGGAG
ACTCAGCCCTTTATCGCTGTGAGTCTGTTGCTCGAAATGACCGCAAGGAATTTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGTGGCGAAGGCTGTACCAAGTGAAGTGGCAACACTG
ACTGCCAGGAGAGTGGAGGCCACCCCGGCTCCTACAGCTGCTATCGCAATGATGTACCACTGCCAGGATT
CCAGAGCCAAATCCAGATTTCGCAATTTCTTCTTCCACTTAAACTCTGAAACAGGCACTTTGGTGTTCAGTGTCTG
TTCACAAAGGACGACTCTGGGCACTACTACTGCATTGCTTCCAATGACGCAAGGCTCAGCCAGGTGTGAGGAGCAG
AGATGGAAGTCTATGACCTGAACATTTGGCGGAATTTATGGGGGGTTCGTGTTGCTTGTGCTGTACTGGCCCTGA
TCACGTTGGGCTCTGCTGTGCTATACAGACGTGGCTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAACCCAGATGGAGTTAACTACATCCGCACTGACGAGGAGGGGCACTTCAGACACAAGTCACTGTTT
TGATCTGAGAGCCCGGCTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTGTCTAGAAACTCTGTCAA
GGCAGCGAGAGCTGATGCATCGGACAGAGCTAGACACTCAITCAGAAGCTTTTCGTTTGGCCAAAGTTGACCA
CTACTCTTCTACTCTAACAGCCACATGAATAGAAGATTTTCTCAAGATGGACCGGTAATATATAACCAAA
GGAAAGCAAACTGGGTGGTTCAGTGAAGTGGGTTCTTAATCTGTTTCTGGCCGTGATTCGCGCATGATATTAGG
GTGATCTTAAAGAGTTTGTCTCAGTGAAGCGCCGCTGCTGGGCCCTGTGAAGCGCAGCACTGTCACCACTGTGCTGT
CAGCAGCCACGACAGCACCATCTGATGGCAGGTTGGCTGGACAGCACCAGCGCATCCCGCGGGAGACCA
GAAAGAGGTTCTTTCACAGCAGGCTTACTTTCATCGGCCACAGACACACCGCAGTTTCTTCTTAAAGGCTCTGCG
TGATCGGTGTTTCAGTGTCCATTGTGGAGAAGCTTTTGGATCAGCACTTTGTAACAAACCAACAAATCAGGAAG
GTAATTTGGTTGCTGGAAGAGGGATCTGCTCAGGGAACCTGCTTGTCCAACAGGGTGTCAAGATTTAAGGAAA
ACCTTCGCTTTAGGCTAAGCTGAAATGGTACTGAAATATGCTTTTCTATGGGCTTGTGTTATTTTAAATTT
TACATCTAAATTTTGTGAAGGTGATTTTGTATTTTGAAGGAAATTTCTATTTAAACTGTAAATATATTGT
TACATAATGTAAATTAACCTATTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAGCTACTACTGTAAAT
TGGAAATATCAATTAATTAAGATATTTTACCAGGAATCCCTCATGGAAGTTTACTGTGATGTTCCTTTTCT
CACACAAGTTTTAGCCTTTTTCACAGGGAAGCTCATACTGTCTACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAAATTTCCAGTTAAGCAATGTTGAAATCAGTTTGATCTCTTCAAAAGAAACCTCTCAGGTAGCTGTGGAAC
CGCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAGGCCCTCAGATGTACATACAGATG
CCAGTCAGCTCCTGGGTTGCGCCAGGCGCCCCGCTCTAGCTCACTGTGCGCTGCTGTGCCAGGAGGCCCT
GCCATCTTGGGCCCTGCGAGTGGCTGTGCTCCAGTGAGCTTACTCAGCTGGCCCTTGTCTCATCCAGCAGAC
TCTCAGGTGGGCACTGAGGGAAGCACTGGTGTCTTCCATGTAGCGTCCGAGCTTTGGGCTCCTGTAACAGACCT
TTTTGGTTATGGATGGCTFCACAAATAGGGGCCCAATGCTATTTTTTTTTTAAAGTTTGTAAATTTATTTGTT
AAGATTGTCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGTCAAGTACAAATCAATTTTTTAAAGAAATGGAT
CCCACTGTCTCTTTGCGCCACAGAGAAGCACCCAGACGCCACAGGCTCTGTCGATTTCAAACCAACCACTGAT
GGAGTGGCGCGCAGTCAGGCTTTTAAAGAACCTCAGGTGGAGCAGCGAGGTGAAGGCTCGGGCGGAGGAAG
TGAACCGCTGAATCAAAGCAGTTTTCTAATTTTGAAGTTTAAATTTTTCATCCGCGGAGCACTGCTCCCATT
TGTGGGGGACATTAAGCAATCACTCAGAAGCTGTGTTCTTCAAGAGCAGGTGTCTCAGCCTCATAGCCCT
GGCGTGTGAGCTCAGGACTGAAGTGTGTAAGCAAGAGCTGCTGAGAAGAGGACCTCACTGTGTGCTGGG
GAATGGCTCTCACTACTCACTTGTCTTTCAGTTCAGTGTCTTGGGTTTTTTATCTTTGACAGCTTTTTTT
AATTTGCAATACATGAGACTGTCTTGAATCTTTTTTAGTATGTGAACACTTTGCGCAGGCGGCTGGCAGAGCA
GGAATGCTCCAGCAGTGGCTCAGTGTCTGCTGCTGCTGCTGCAATGGCATCTCGATGCTTAGCATGCAAGTTC
CCTCATCTATTGCCACTTGGTAGAGAGGATGGCTCCCACTCAGGCTGGGGGATTCAGCTCCAGCTCCTCT
TCTTGGTTGTCTAGTGTATAGGTAGCCCTATTGCCCTCTCTTATACCTTAAACCTCTACATAGTGGCA
TGGGAACAGGCTCTGAAAGTGTGAGAGAAGTGAAGTGAAGTCTGGGAAGTGTGCTATTAAGCTGAGACTG
CGGAAAGCAATATCTGTGATTTTAAATATGAATGTGACTCAAGACTCGAGGCCGATACAGGCTGTGATTC
CCTTTTGGATGATGCTGTGTACAGATGCTACAGACTGTACTAACACACCGTAATTTGGCATTTGTTTAAAC
CTCATTTTAAAGCTCTCAAAAAACCA

538/550

FIGURE 538

MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTS DP
RIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTS LKIWNVTRRDSALYRCEVVARNDRKEI
DEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQES EGHPRPHYSWYRNDVPLPTDSRANPR
FRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYVDLNIGGIIGGVLVV
LAVLALITLGICCAYYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features:**Signal peptide:**

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

539/550

FIGURE 539

CCAGGACCAGGGCGCACCGGCTCAGCCTCTCACTTGTCAGAGGCCGGGGAAGAGAAGCAAAGC
GCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCTAA
CTTCAGTCCCCCAAACCGGCGACCCTCGAAGTCTTGAAC'TCCAGCCCCGCACATCCACGGCGCG
CACAGGCGCGGCGAGCGCGCAGTCCCGGCCGAAGCGCATGCCGCGCAGGGGTCGGGCGAGCTGG
GCTCGGGCGCGCGGAGTAGGGCCCGGCGAGGGAGGCAGGGAGGCTGCATATTAGAGTTCGGGG
CTGCGCCCTGGGCGAGAGCGCGCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCGCGCGCA
TGAGCCGCGCTGGTCTCGCTGCTGCTGGGCGCGCGCTGCTGCTCGCGCCACGGAGCCTTCTGCC
GCCGCGTGGTCAGCGGCCAAAAGGTGTGTTTTGTGCTGACTTCAAGCATCCCTGCTACAAAATGG
CCTACTTCCATGAAC'TGCCAGCCAGTGAAGCTTTCAGGAGGACCGCCTGGCTTGTGAGAGTG
AGGGAGGAGTCTCTCAGCCTTGAAGATGAAGCAGAACAGAAAGTGAATAGAGAGCATGTTGC
AAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGGGCTTTGGAGGA
ATGGAGATGGGCAACATCTGGTGCTGCCAGATCTCTACCAGTGGTCTGATGGAAGCAATT
CCCAGTACCGAAACTGGTACACAGATGAACCTTCTCGCGGAAGTGAAGTGTGTTGTGATGT
ATCACCACCAACTGCCAATCCTGGCCTTGGGGTGCCCTACCTTTACCAGTGGAAATGATGACA
GGTGTAACATGAAGCACAAATATATTGCAAGTATGAACCAGAGATTAATCCAAAGCCCTCG
TAGAAAAGCCTTATCTTACAAATCAACCAGGAGACCCATGAGTGTGGTGTGTTACTGAAG
CAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAAAATACCCCTGCTCTTACTGATAC
TGGTGTGCTTTTGGAACTGTGTTTCCAGATGCTGCATAAAAGTAAAGGAAGAACAAAACATA
GTCCAAACCGACTACACTGTGGATTTCAAAGAGTACCAGAAAAGAAAGTGGCATGGAAATG
AAATAACTCATTGACTTGGTTCAGAAATTTTGTAATCTGGATCTGTATAAGGAATGGCATCAG
AACAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGCAAGATGAAGTGAAGCTCCCCCT
TGAGGCAAAATATTAAGTAATTTTTATATGTCTATTATTTCAATTAAGAAATATGCTGTGCTA
ATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCACCCAAACTTCAAACCTCAAGCAAA
TGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTCGGGAGTATGTGTGTTAGAAGCAAT
TCCTTTATTTCTTTCACTTTTCATAAGTTGTTATCTAGTCAATGTAATGTATATTGTATTGA
AAATTTACAGTGTGCAAAAGTATTTTACCTTTGCATAAGTGTGTTGATAAAAATGAAGTGTCTA
ATATTTATTTTATGGCATCTCATTTTTCATATACATGCTCTTTTGATTAAAGAACTTATTAC
TGTTGTCAACTGAATTCACACACACACAAATATAGTACCATAGAAAAAGTTTGTTTCTCGAA
ATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCAATGTCTAGGAAATCTCTTCAGAAATAAGA
AGCTATTTCCATTAAGTGTGATATAAACCTCCTCAAACATTTTACTTAGAGGCAAGGATGTCT
AATTTCAATTTGTGCAAGACATGTGCCTTATAAATTTTTCAGCTTAAATTAACAGATTTTG
TAATATGTAACTTTGTTAATAGGTGCATAAACACTAATGCAGTCAATTTGAACAAAAGAGT
GACATACACAATATAAATCATATGTCTTACACGTTGCCATATAATGAGAAGCAGCTCTCTG
AGGGTCTCGAAATCAATGTGGTCCCTCTCTTGCCCACTAAACAAAGATGGTTGTTCTGGGGTTT
GGGATTGACACTGGAGGCGAGATAGTTGCAAGTTAGTCTAAGGTTTCCCTAGCTGTATTAGC
CTCTGACTATATTAGTATACAAAGAGGTCAATGTGGTTGAGACCAGGTGAATAGTCACTATCAG
TGTGGAGACAAGCACAGCACACAGACATTTAGGAAGGAAAGGAAC'TACGAAATCGTGTGAA
ATGGGTTGGAAACCATCAGTGATCGCATATTCATTGATAGGGTTTCTTGTAGATAGAAAATG
GTGGCTCCTTTCTGTCTTATCTCCTAGTTTCTTCAATGCTTACGCTTGTCTTCTCAAGAGA
AAGTTGTAACTCTCTGTGCTCATATGTGCTCCTTTTAAACCAATAAAGAGTCTTCTG
TTTCTGGGGGAA

540/550

FIGURE 540

MSRVVSLLLGAALLCGHGAFCRRVVSQGKVCFADFKHPCYKMAFYHELSSRVSFQEARLACES
EGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDWFIGLWRNGDGGTSGACPDLYQWSDGSN
SQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWDDRCNMKHNYICKYEPEINPTAP
VEKPYLTNQPGDTHQNVVTEAGIIPNLIYVVIPTIPLLLLLILVAFGTCCFQMLHKSKGRKTK
SPNQSTLWISKSTRKESGMEV

Important features:**Signal peptide:**

amino acids 1-21

Transmembrane domain:

amino acids 214-235

N-glycosylation sites.

amino acids 86-89 and 255-258

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 266-269

N-myristoylation sites.amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145
and 212-217

541/550

FIGURE 541

GGAGAATGGAGAGAGCAGTGAAGTGGAGTCCGGGGTCTGGTCGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG
 CCACAGCCACTGGGGCCCAAGTTGTCTCAGCCTGAAAGTAGACACACCCCTGGGTGCTGCGGAGGCGGCGAGGTGG
 GCGTGAGGGGCACACACCGCTTGTGAATGTCTTCTGGGCATTTCATTTCGCCAGCGCCCACTGGGGCTTGACC
 GGTCTTCCAGCCCCACACCCAGCAGCAGCCTGGGAGGGTGTGCGGGATGCCAGCAGCTCGCCGCCCAATGTGCGCTAC
 AAGACGTGGAGAGCATGAACAGCAGCAGATTGTCTTCAACGGAAACAGCAGATCTTCTCGCTTTCAGAGAGT
 GCCTGGTCTCAACGTCTATAGCCAGCTGAGGTCCCGCAGGGTCCGGTAGGGCCGTATGGTATGGGTCCATG
 GAGGCGCTGTATACTGGCGTGCACCTCTCTACGATGGATCAGCTCTGGCTGCCATGGGATGTGGCTCTGG
 TTACAGTCCAGTACCGCTTGGGTCTTGGCTCTTTCAGCAGCTGGAGATGAGATGCACCTGGCAACCGAGGT
 TCTTAGATGTGGTAGCTGCTTTGGCTGGGTGCAGAAAACATCGCCCCCTTCGGGGGTGACCTCAAGCTGTGTCA
 CTGTCTTTGGTGGATCGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGGTGCGAGGGCTGTTCC
 ACAGAGCCATCACACAGAGTGGGGTCACTACCACCCAGGGATCATCGACTCTCACCTTGGCCCCTAGCTCAGA
 AAATCGCAACACCTTGGCTGCAGCTCCAGCTCCCCGGCTAGAGTGGTGCAGTGCCTTCAGCAGAAAGAGGAG
 AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATATATCTATCTCTCACCCTTGATGGCACTGTCTTCCCCAAAA
 GCCCCAGGAACTCCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTTCA
 GCTGGCTCATCCCCAGGGGCTGGGGTCTCTGGATACAAATGGAGCAGATGAGCGGGAGGACATGCTGGCCATCT
 CAACACCCGCTTGAACCTGTGGATGTGGCTTGCCTTCAGATGATGCCACCGCTCATAGATGAATACCTAGGAAGCA
 ACTCGGACGCACAGCCAAAGTCCAGGCGTTCAGGAATTCATGGGTGACGTATTCTCATATGTTCCACCCGTCA
 GTTTTTCAGATACCTTCAGAGATTCTGGGAAGCCCTGTCTTTTCTATGAGTTCAGCATCAGCCAGCTTCTTTTG
 CGAAGTCAAACTCCCTGGTGGTGAAGGCTGATCATGGGCGAGGGTGCTTTTGTGTCGGAGGTCCCTTCTCA
 TGGCAGAGAGCTTCCGCTCGCCCTTTTCAGAGGCCACAGAGGAGGAGAAGCAGCTAAGCCTCACCATTGAGTGGCC
 ATGGGACCCATTTCGCCGACAGCGGACCCCAATAGCAAGGCTCTGCTCTTGGGCCCAATTCAACAGGGCGG
 AACATATCTGAGATCAACCAAGTGCACCGGGCCGACAGAAAGTTACAGGAGGCCCTGGATGCATCTTGGTCAG
 AGACCTTCCCGCAGATACCAAGCTGGCACCGAAGCAGAAAGACGAGGAGGCCACAGGAGACCTCTCGGACCC
 AGGCTGAACTCTTGTGGCTGGGCGAAACCACTCTCAAGTGGTGGCAGAGTCCCGACCGGCACGCCCGCTCTC
 CCGCTGTGAGACTTAACTCTCACAGCCCTTAAAGTGTGCGCGCTCTGTGACTGGATGTATGCTCTTTTGA
 ATGTCACAAGCGCGCTCCCACTCTGGGCAATTGACAAGTCTTCCCTCTCCCTGAAGTGCCTTCTCGTCTT
 TCTCGTGGTAGGTTCTAGACATTCTCTAGCTTCTTGGAGGACTCACTCCCGAGGAAGCCTTCCCTGCCTCTCT
 TGGGCTGTGCGGCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT
 CCCCCCTCAGAGGAGCTCTCTCAAATGGGGATTAGCTTAACCCCACTCTGTCAACCCACACAGGATCGGGTGGGA
 CCTGGAGCTAGGGGTGTTTGTCTGAGTGAAGTGAACACAGAAATATGGGAATGGCAGTCTGAACTTGAAC
 CCAGAGCCTTCAGGTGGCAAAAGCCATACTCAGGCCCCACCGACATTGTCCACCTTGGCCAGAAGGGTGCATGCC
 AATGGCAGAGACTGGGATGGGAAGTCTTGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCTGAC
 TAAGGCTCTAGACTAGGGCGGGAGGGGTCTCTCTCTCTGTCTGCTGCCAGTCTTGGCCCCGACACAAGACACAGA
 ATCCACTCAGGGGCTAGTGTCTCACCCAGACCTTGACCTTCAACAATCCAGCCCTGACCTCAGGAGCTGGATG
 CCAGCTCCCCAGCCCAAGTGGCGGGTCTCTCTCTCTCTGCTTGGGAGACAGGATTTCTGGGAGGCTTCCAAG
 AGCACAACCAAGACACAGCAGGACAGGCCAGGGGAGGCGATCTGGACAGGCACTCCGTCCGGCATTTGTCTACA
 GAGAAAGACAGAGACCCCACTCGGGCTGCAAAAGGTGAAAGCACCACAGAGGTTTTCAGATGGAAGTGAAG
 GTGACAGTGTGCTGGACCCCTCAGACGCTCTGCTGTCTCTCCCTGCGCGCTCTGCTGGGCTCCCACTTTGGGA
 GCATCTGAGGAGCCCTCAAGCCGCGCTGCACTGTAGGAGCCCTTTCTGGGCTGGCCAAAGGCGAGGCCGCT
 CCGTCAAGCTTTCGGGGAGGCTGCGGAGGGAGAGGGCGGGCAGGAACCGGGCTGCGCGCAGGCTTTCGGGGCAG
 AGTGAATTCCGGTGGGCTGGGCTGCGCGGGGCCCACTCAGAGCAGCTCAGGCGCCCGAGGCAAGTGGGCTCT
 TAGCACTGGGCGGACAGCTGCTGTCTGCTGATTTCTCGTGGGCTTGTAGCTGCTCCCCGCGGGCAGGGCTCGG
 GACCTGACGCTTCCATGCTTGACCTTCCCCACCCCGCTGCGGCTCTGTGGCGCGGAGCTTCCCCAAGAG
 CGCGCGCCCTGCTCTGACAGCGCCAGTCCCTCAGACCCCAAGGCTGTAGGAGTGGGGGTGACAGCGCGGGA
 TCCGACGGCAGCTCCACTCTGCCCCAGTGTCTGGATCCACTGGTGAAGCTGAGTGGCTGCTGAGTCTGGTGG
 GGACTTGGAGAACCTTATGTCTAGCTAAGGGATTGTAATACACCGATGGGCATCTGTATCTAGCTCAAGGTT
 TGTAAACACCAACATCAGCACCTGTGTCTAGCTCAGTGTGTGTAATGACCAATCCACATCTGATCTGTGCT
 ACTCTGGTGGGCACTTGGAGACCTTTGTGTCACACTCTGTATCTAGCTAATCTAGTGGGAGTGTGGAGAACCT
 TTGTGTTCTAGCTCAGGGATCTGAAGACGCCAATCAGCACCTCTGTCAAAACAGACCACTTGACTCTGTGTAAT
 GGACCAATCAGCAGGATGTGGTGGGGCGAGACAGAGAATAAAGCAGGCTGCTGAGCCAGGATGACAAACC
 CCCTCGGGTCCCTCCACGCGCTGGAAGCTTTGTTCTTTCGCTCTTTGCAATAAATCTTGCTACTGCCAAAA

542/550

FIGURE 542

MERAVRVESGVLVGVCLLLACPATATGPEVAQPEVDTTLGRVRGRQVGKGTDRLVNVFLGI
PFAQPPLGPDRFSAPHPAQPPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDCLV
LNVYSPAIEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAYGDVVVVTVQYRLGVLGFFSTG
DEHAPGNQGFLDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIISGLVLSPVAAGLFHRAI
TQSGVITTPGIIDSHWPPLAQKIANLTLACSSSSPAEMVQCLOQKEGEELVLSKKLKNTIYPLT
VDGTVFPPKSPKELLKEKPPHSVPFLMGVNNHEFSWLI PRGWGLLDTMEQMSREDMLAISTPVL
TSLDVPPEMMPTVIDEYLGNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGSPVFFYEF
QHRPSSFAKIKPAWVKADHGAEGAFVGGPFLMDESSRLAFPEATEEEKQLSLTMMQAQWTHFA
RTGDPNSKALFPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQWHQKQKNRKA
QEDL

Important features:**Signal peptide:**

amino acids 1-27

Transmembrane domain:

amino acids 226-245

N-glycosylation site.

amino acids 105-109

N-myristoylation sites.

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,
461-467

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 12-23

Carboxylesterases type-B serine active site.

amino acids 216-232

543/550

FIGURE 543

TGTGCGCTTGGCCCTCGCC**ATG**CAGACCCCGGAGCGTCCCTTCCCGCCGGGCCCTCCTGCTTCTGCTGCTGCTA
 CTGGGGGGCGCCACGGGCTCTTTCCTGAGGAGCCGCCGCCCTTAGCGTGGCCCCAGGGACTACCTGAACACAC
 TATCCCGGTGTTTGTGGGAGCGGGCCCGACGCTTGACCCCGCAGAAAGTCTTGACGACCTCAACATCCAGGGA
 GCTCTCGGGGTCAACAGGACGCTGTTTCATTGGGGACAGGGACAACCTCTACCGGCTAGAGCTTGAGCGTCCCCACG
 TCCACGGAGCTCGGTACAGAGGGAAGTCACTTGGAGATCTAACCCNAGCGACATAAAGCTGTGGATGAAG
 GGCAACAGGAGGGCGAGTGTGAAACTTCGTAAGGTGCTGCTCTTCGGGACGAGTCCACGCTCTTTGTGTGC
 GGTTCACAGCGCTTCAACCCGGTGTGGGCCAATACAGCATAGACACCTCGAGCCGCTCGGAGACAAATACAGC
 GGTATGGCCCGTGTGGGACGCGGCCGAGCAGCCCAATGTTGCCCTCTTCTTGACGGGATGCTCTTCAACGCT
 ACTGTTACGCACTTCTTACGCACTTGATGCTGTCACTACCGCAGGCTCGGGGACAGGCCACCCCTCGCGACCGGTG
 AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGACGCCATGTCTACTTCTTC
 TCCCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCCGCTGGCCCCGAGTGTGCAAGAAC
 GACGTGGGAGGCTCCCCCGCTGCTGGAGAAAGCAGTGGAGCTCCTTCTTCAAGGCGCGGCTCAACTGCTCTGTA
 CCGGAGACTCCCATTTCTACTTCAACGTGCTGACGGTGTCAAGGCGTGGTCAAGGCGTGGTCAAGGCGCGGCCGCTG
 GTCTGGCCGCTTTTTCACAGCCACAGCAACAGCATCCCTGGCTGGCTGTGCGCTTTGACCTGACACAGGTG
 GCAGCTGTGTTTAAAGGCCGCTTCCGAGAGCAGAAGTCCCGGAGTCCATGTGAGCGCGGTGCCGAGGATCAG
 GTGCTCGACCCCGGCCCGGCTGCTCCGACGCCCGGGGATGCAGTACAACTGCTCCAGCGCTTGGCGATGAC
 ATCCTCAACTTTGTCAAGACCCACCCCTCTGATGGACGAGGCGGTGCCCTCGTGGCGCATGGCCCTGGATCCTG
 CGGACCTCGATGAGGACACAGCTGACTCGAGTGGCTGTGGAGCTGGGAGCGGCCCTCGGGCAACACAGACCGTT
 GTCTTCTGGGTTCTGAGGCGGGGAGCGTCCCTCAAGTTCTCTCGTCCGCCCAATGCCAGCACTCAGGAGGCTCT
 GGGCTCAGTGTCTCTCTGGAGAGTTTGAGACCTACCGGCCGAGCAGGTGTGGAACGGCCCGGCGGTGGCGAGAGC
 GGGCAGCGCGCTCTGAGCTTGGAGCTGGAGCGCAGCTTCGGGGGGCTCTGCTGCTTCCCGCTGCTGCTGTC
 CGAGTGCCTGTGGCTCGCTCGCTCGACAGTACTCGGGTGTATGAAGAACTGTATCGCAGTCAAGGACCCCTACTGCG
 GGGTGGGCCCCGACCGCTCTCAGCTTCTCTCAGCCCGGGCACCAGAGCGCTTTGAGCAGACGTGTCCCGGG
 GCCAGCACTCAGGCTTAGGAGCTGCACAGGACTCCTGCGGGCAGCCTTCCGAGGACCGCGCGGGCTGGTG
 TCGGCAACCTCGTGTAGGCTGCTGGTGGCGGCTTCTGTTGGAGCGCTGTGCTGCGGCTTGGCTGCGGCTGGG
 TGGTTCGTGGGCTCCCTGACCGCGGGAGCTGGCCCGCGCAAGGACAAAGAGGCCATCTTGGCGCACGGGGCG
 GGGAGGCGGTGCTGAGCGCTCAGCGCTCGGCCGAGCGCAGGCGCAGGCTTCCGGGGCGCGGGCGGAGGCGGT
 GGGGTGGCGCGGGGTTCCCCCGGAGGCCCTGTGTCGCCCTCTGATGCAGAACGGCTGGGCAAGGCCACGCTG
 CTGACGGGCGGGCCACAGCACTGGACTCGGGCTGCTGCCACGCCGAGCAGAGCGCGCTGCGCGAGAAGGGC
 CTGGCCACTCCGCAACCGCACCCCCACGCGCTTGGGCCCCGCGGCTGGGACACAGGCCACCCCTGCTCCCGGCC
 TCCGCTTCATCTCCTCCTGCTGCTGGCGCCGCGCGGCCCGGACGAGCCCCCGGCTCGGGAGCGGACG
 CCGACGCGCGCTCTATGCTGCTCGGGCCCGGCGCGGCTTCCACGGGAGCTTCCGCTCACCCCACGCCAGC
 CCGAGCCGCGCGGCTGGTGTCCGCGCCACGGGCCCTTGGACCCAGCTCAGCGCCGATGGCTTCCCGGG
 CCGTGGAGCCCGCCCCGACGGGACGCTGAGGAGGCCACTGGGCCCCACGCCCTTCCGGCGGACACTTCCGCG
 CGCACCCACAGCTTCAACAGCGGCCAGGCGCGGCTGGGACCGCCACCGCGGCTGCCACCGCGCGCGGGGACAC
 GACTTGCCCACTCTCCCTATGGGGGGCGGACAGGACTGCGGCCCGCGCTG**AGG**CGCGGGGGCCCCCG
 ATGCTTGGCAGTGCCAGCACGGGAACAGGAGCGAGACGCTGCCAGAAGCGCGGGGCCGGGGCACTCCG
 AGTGGGTCTCAAGTCCCCCGCGACCCACCGCGAGTGGGGGGCCCCCTCGGCCACAAGGAAGCAACACACG
 CTCGCCCTCCCTTCCCGGGGCCGAGCAGCGTGAGACGTTTGGGGTGGTGGCGGGAGGACTTCTGTATG
 GATTGAGGTTGACCTTATCGCGGTAGTTTTGGTTTTTTTCAGTTTTGGTTTCTTTTCGGTTTTCTCAACC
 AATTGACAACTTCGTTCTCGGGGTGGCGGACGAGGGGAGGCTTGGACGCCGTTGGGAATGGGGGGACAG
 CTGCAGACCTAAGCCTTCCCGACCCCTGGAAGGTCCCTCCCAACCAAGGCCCTTGGCGTGTGGGTGTGGC
 TGGCTGTGCTGCGGTGTTGCTGTGCAAGGGCGGGAGGTGGCGTGTGTGCTGCTGCCAGCGAAGGCTGCTG
 TGGGCGTGTGCTCAAGTGGGCCACGCTGCAGGGTGTGTGTCCAGAGCGACGATCGTGGTGGGCCCCAGCGGCC
 TGGCGTGTGGCTGAGCGAGCGCTGGGGCTTCCAGAAGGCCCGGGGTTCAGAGGTGCGGTTAGAGTTTGAAC
 CCCCCCACTCTGCAAGAGGAAGCGGGACAATCCCGGGTTTCAAGCAGGACACAGGAGAGGCCCTGCCCGGA
 ATGCATATCGGACGAGCTGTCTAAGGGCTTGGGGGCTTGGGGGGCGGAGAGTGGTGGGGCCCTCTGTAA
 AGCGGCCCGAGGTTGGTGAAGAGTCCATGACACCGCTCCCTTGTGACCTCCCCCTATGACCTTCAAGCTGA
 CCATCCATGCCACTGTGCTGGCTGGGTCTCTGCTCTTCTTGGAGTTTGGCTCCCCCGACCGCTCCCCATCAAT
 AAAACTCTGTTTACAAACAAAAA

544/550

FIGURE 544

MQTPRASPPRPALLLLLLLLGGAHGLFPPEPPPLSVAPRDYLNHYPVFVSGSGPGRLLTPAEGAD
 DLNIQVRVLRNRTLFIGDRDNLRYVELEPPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEGEC
 RNFVKVLLLLRDESTLFVCGSNAFNPCANYSIDTLQPVGDNISGMARCPYDPKHANVALESDG
 MLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWEKEPYFVHAVENGSHVYFFFREIAMEF
 NYLEKVVVSVRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSPVPGDSHFYFNVLQAVTGVVSLG
 GRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTFPVEDQVPRPRPGCC
 AAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVAVDVGAGPWGN
 QTVVFLGSEAGTVLKFLVRPNASTSGTSGLSVFLEEFETYPDRDCRPGGGGTGQRLLSLELD
 AASGGLLAAFPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPGTRAAFEQDV
 SGASTSGLGDCGTGLLRASLSEDRAGLVSNNLVTSSVAAFVVGAVVSGFSVGWVGLRERREL
 ARRKDKAEILAHGAGEAVLSVSRLGERRAQGPGGRGGGGGGAGVPPEALLAPLMQNGWAKAT
 LLQGGPHDLDLSGLLPTPEQTPLPQKRLTPHPPHAPALGPRAWDHGHPLLPASASSLLLLAPA
 RAPEQPPAPGEPTDGRLYAARPGRASHGDFELTPHASPDRRRVVSAPTGELDPASAADGLPR
 PWSFPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPGTDLAHLFPYGGADR
 TAPPVP

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 318-339, 598-617

N-glycosylation sites.

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,
462-466

Glycosaminoglycan attachment sites.

amino acids 51-55, 573-577

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation sites.

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,
668-674, 669-675, 670-676, 868-874, 879-885

545/550

FIGURE 545

GATGGCGCAGCCACAGCTTCTGTGAGATTGCGATTTCTCCCCAGTTCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA
ACAAGTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGACAGAATAAAGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTCACGGGAG
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAGGCCTAAGATGAAAGCCTCTAGT
CTTGCCCTTCAGCCTTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAGATGGAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTACAGATTCTTCTGCAATGGATGGAG
GAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTGTGAATATCTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTGTATTTAATGTAITTTATTTTTTACTTGGACATG
AAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTAT
ACAGTAAAAAAGAAACCTTGTAATTTCTAGAAGAGTGGCTAGGGGGGTTATTCAATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTGTGGAATAAGTTTGTATGTGAATGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAAATTGTGTATCTTCCAGCCAGGAATCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATACCAAAAAAAAAAAAAAAAAAAAA

546/550

FIGURE 546

MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRPE
IFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNLQE
IRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTPDHY
TLRKISSLANSFLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALGELDI
LLQWMEETE

Important features:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

547/550

FIGURE 547

AGCAACTCAAGTTCATCATTGTCTCTGAGAGAGAGAGCAGCGCGGTTCTCGGCCGGGACAGCA
GAACGCCAGGGGACCCTCACCTGGGCGCGCCGGGCGACGGGCTTTGATTGTCTCTGGGGTCGCG
GAGACCCGCGCGCCTGCCCTGCACGCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTGCGA
TCGSCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTTCATT
ATCGGTGGATCATTTTCGAGAGTCCGCTTTGTAAATGTTTGGCACTTTGTCTACTTTATTGCTTC
TTTCTGGCGACAGTTCAGCACTCGCCGAGACCGCGGAGAAAGGCAGCTGAGCCCGGAGAAG
AGCGAAATATGGGACC CGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTTCTATATT
CAGGCAGTGGATACATCAGGGAATAAATTACATCTTCTCCAGGCGAAAAGGTCTTCCAGGTG
AAAGTCTCAGCACCAGAGGAGCAATTCAGTAGAGTTGGAGTCCAGGTTTTAGACCGAAAAGAT
GGGTCTTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGTGGAAATTAAA
TTCCAAGGGCAACATGTGGCCAAATCCCCATATATTTTAAAAGGGCCGGTTTACCATGAGAAC
TGTGACTGTCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAAGTGCCTGAAACCATT
GCTCAGATTTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAAGATTGCAGTAGAA
ATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGCTACTACACCTTAAAGGATAACAAGGTT
TATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTCATGGATGCCATACTACTTTCT
TTGACTAGAAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTTGGGAGACTGGCCTTTG
GAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCTGGTGTGGCTCCACAGATTCC
AAGGATATCGTGATGCCCTACGTACGATTTGACTGATTCTGTTCTGGAAACCATTGGGCCGGGTA
AGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCTCCCTGGGAAAGCAAAAATTCCTACT
GCCGCTCTGGAGAGGGCGAGACAGCCGCAAGAGAGACTCGAGCTGGTTAACTCAGTAGAAAA
CACCAGAACTCATAGACGCTGCTTTTCCCAACTTTTTCTTCTTTAAACACGATGAAAACCTG
TATGTTCCCATTTGTGAACATATTTTCATTTTTTGATTTCTTCAAGCATAAGTATCAAATAAAT
ATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGCTAGTTGGTGACAGTGTTGTGCTG
AAGCAGGATTCCATCTACTATGAACATTTTTACAATGAGCTGCAGCCCTGGAAACACTACATT
CCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAAACTTAAATGGGCGAAGATCACGATGAA
GAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTGCAAGAAATAATCTCATGGGCGATGAC
ATATTCTGTTATTATTTCAACTTTTCCAGGAATATGCCAATTTACAAGTGAGTGAGCCCCAA
ATCCGAGAGGGCATGAAAAGGGTAGAACCACAGACTGAGGACGACCTCTTCCCTGTACTTGC
CATAGGAAAAAGACCAAGATGAACCTGATATGCAAAATAACTTCTATTAGAATAATGGTGC
TCTGAAGACTCTTCTTAACTAAAAAGAAGAATTTTTTAAAGTATTAAATCCATGGACAATATA
AAATCTGTGTGATTGTTTGCAGTATGAAGACACATTTCTACTTATGCAGTATTCTCATGACTG
TACTTTAAAGTACATTTTTAGAATTTTATAATAAAACCACCTTTATTTTAAAGGAAAAAA

548/550

FIGURE 548

MFGTLLLYCFFLATVPALAEETGGERQLSPEKSEIWGPGLKADVVLPAFYFYIQAVDTSGNKFT
SSPGEKVVFQVKVSAPEEQFTRVGVQVLDKDGSFIVRYRMYASYKNLKEIKFQGGHVAKSPY
ILKGPVYHENCDCPLQDSAAWLREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRFQGRQSL
CHYTLKDNKVYIKTHGEHVGFRIFMDAILLSTRKVKMPDVELFVNLGDWPLEKKKSNSNIHP
IFSWGCGSTDSDKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVVWRGRDSRKE
RLELVKLSRKHPELIDAAFTNFFFFKH DENLYGPIVKHISFFDFFKHKYQINIDGTVAAYRLP
YLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKS NLSDLLEKLKWAKDHDEEAKKIAKAGQE
FARNNLMGDDIFCYYFKLFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRKKTKDEL

Important features:**Signal peptide:**

amino acids 1-17

N-glycosylation sites.

amino acids 302-306, 414-418

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 243-247, 495-499

Tyrosine kinase phosphorylation site.

amino acids 341-348

N-myristoylation sites.

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

Endoplasmic reticulum targeting sequence.

amino acids 499-504

549/550

FIGURE 549

GGGTGATTGAACTAAACCTTCGCCGCACCGAGTTTGCAGTACGCGCCGTACCCGCACCGCTGC
CTGCTTGCGGTTGGAGAATCAAGGCCCTACCGGGCCTCCGTAGTCACCTCTCTATAGTGGGC
GTGGCCGAGGCCGGGGTGACCTGCCGGAGCCTCCGCTGCCAGCGACATGTTCAAGGTAATTC
AGAGGTCCGTGGGGCCAGCCAGCCTGAGCTTGCTCACCTTCAAAGTCTATGCAGCACCAAAAA
AGGACTCACCTCCCAAAAATCCGTGAAGTTGATGAGCTTTCACCTACTCAGTTCCTGAGG
GTCAATCGAAGTATGTGGAGGAGCAAGGAGCCAGCTTGAAGAAAGCATCTCACAGCTCCGAC
ACTATTGCGAGCCATACACAACCTGGTGTGAGGAAACGTACTCCCAACTAAGCCCAAGATGC
AAAGTTTGGTTCAATGGGGGTTAGACAGCTATGACTATCTCCAAAATGCACCTCCTGGATTTT
TTCCGAGACTTGGTGTATTATGGTTTTGCTGGCCTTATTGGACTCCTTTTGGCTAGAGGTTCAA
AAATAAAGAAGCTAGTGTATCCGCCCTGGTTTCATGGGATTAGCTGCCTCCCTCTATTATCCAC
AACAAGCCATCGTGTTTGCCAGGTCAGTGGGGAGAGATTATATGACTGGGGTTTACGAGGAT
ATATAGTCATAGAAGATTGTGGAAGGAGAACTTCAAAGCCAGGAAATGTGAAGAATTCAC
CTGGAACTAAGTAGAAAACCTCCATGCTCTGCCATCTTAATCAGTTATAGGTAAACATTGGAAA
CTCCATAGAATAAATCAGTATTTCTACAGAAAAATGGCATAGAAGTCAGTATTGAATGTATTA
AATTGGCTTTCTTCTCAGGAAAAACTAGACCAGACCTCTGTTATCTTCTGTGAATCATCCT
ACAAGCAAATAACCTGGAATCCCTTCACCTAGAGATAATGTACAAGCCTTAGAACTCCTCAT
TCTCATGTTGCTATTTATGTACCTAATTAAACCCCAAGTTTAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAA

550/550

FIGURE 550

MFKVIQRSVGPASLSLLTFKVYAAPKKDSPPKNSVKVDELSLYSVPEGQSKYVEEARSQLEES
ISQLRHYPEPYTTWCQETYSQTKPKMQSLVQWGLDSYDYLQNAPPGFFPRLGVIGFAGLIGLL
LARGSKIKKLVYPPGFMGLAASLYYPQQAIVFAQVSGERLYDWGLRGYIVIEDLWKENFQKPG
NVKNSPGTK

Important features:**Signal peptide:**

Amino acids 1-23

Transmembrane domain:

Amino acids 111-130

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 26-30

Tyrosine kinase phosphorylation site:

Amino acids 36-44

N-myristoylation sites:

Amino acids 124-130;144-150;189-195